



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/673,840

Source: PCT 09

Date Processed by STIC: 2-15-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/673,840

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) \_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) \_\_\_\_ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) \_\_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/673,840

DATE: 02/15/2001  
TIME: 14:19:53

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

5 <110> APPLICANT: metaGen Gesellschaft f?r Genomforschung mbH (Assignee)  
7 <120> TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue  
9 <130> FILE REFERENCE: 51587AWOM1XX24-P  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,840  
C--> 12 <141> CURRENT FILING DATE: 2000-10-23  
14 <160> NUMBER OF SEQ ID NOS: 431

## ERRORED SEQUENCES

11006 <210> SEQ ID NO: 416  
11007 <211> LENGTH: 144  
11008 <212> TYPE: PRT  
11009 <213> ORGANISM: homo sapiens  
11011 <400> SEQUENCE: 416

E-->	11013	Tyr	Thr	Met	(Xxx)	Ile	Ile	Tyr	Phe	Thr	Arg	(Xxx)	Ile	Leu	Tyr	(Xxx)	Gln
	11014	1				5					10				15		
E-->	11016	Gly	Gly	Ile	Leu	Lys	Tyr	Asn	Thr	Pro	Gly	(Xxx)	Ser	Phe	Leu	Leu	Tyr
	11017				20					25					30		
E-->	11019	Ile	Met	Ile	Val	Ser	Phe	His	Ile	Ser	Trp	(Xxx)	Leu	(Xxx)	(Xxx)	Gly	Lys
	11020				35					40				45			
E-->	11022	Gly	Thr	(Xxx)	Lys	Ser	Ile	Phe	Ile	Tyr	Ile	Lys	Thr	Lys	(Xxx)	(Xxx)	Gln
	11023				50					55				60			
E-->	11025	(Xxx)	Arg	Leu	(Xxx)	Pro	Pro	Lys	Cys	Leu	Val	Ser	Leu	Glu	Asn	Asn	Met
	11026				65			70			75						80
E-->	11028	Asn	Glu	(Xxx)	(Xxx)	Lys	Met	Asn	Gln	Ile	Thr	Trp	(Xxx)	Thr	His	Arg	Arg
	11029					85					90				95		
E-->	11031	(Xxx)	Asn	Lys	(Xxx)	Ala	Gln	Glu	Ile	Lys	Ser	Cys	Phe	Lys	Leu	Gly	His
	11032				100					105					110		
	11034	Ile	Lys	Gly	Lys	Lys	Gly	Ser	Glu	Arg	Arg	Val	Arg	Lys	Ile	Ser	Ser
	11035				115					120				125			
E-->	11037	Gln	Ala	Thr	Lys	Asn	Leu	(Xxx)	Arg	Arg	Gln	Pro	Pro	Asn	(Xxx)	Ile	Arg
	11038				130			135					140				

11040 <210> SEQ ID NO: 417  
11041 <211> LENGTH: 74  
11042 <212> TYPE: PRT  
11043 <213> ORGANISM: homo sapiens  
11045 <400> SEQUENCE: 417

E-->	11047	Leu	Ile	Leu	Met	Gly	Arg	Leu	Ile	Tyr	Asn	(Xxx)	Asn	Tyr	Leu	Phe	Tyr
	11048	1				5					10				15		
E-->	11050	Lys	(Xxx)	Asp	Ser	Ile	His	(Xxx)	Gly	Arg	His	Leu	Glu	Val	Gln	Tyr	Thr
	11051				20					25					30		
E-->	11053	Arg	(Xxx)	Phe	Ile	Ser	Ser	Leu	His	Tyr	Asp	Cys	Glu	Phe	Pro	Tyr	Lys
	11054				35				40					45			
E-->	11056	Leu	(Xxx)	Thr	(Xxx)	His	(Xxx)	Lys	Gly	Asn	(Xxx)	Lys	Ile	His	Phe	Tyr	Ile
	11057				50			55					60				
E-->	11059	His	Lys	Asn	Lys	Thr	(Xxx)	Pro	(Xxx)	Glu	Thr						

Invalid amino acid designator.  
Xxx should be Xaa. Sequences  
containing "Xaa's" or "n's" must have  
<220> to <223> features to explain  
what they represent.  
(They may only represent  
a single residue.)  
See #10  
on the  
Error  
Summary  
Sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/673,840

DATE: 02/15/2001  
TIME: 14:19:55

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

11060 65

70

<210> 391  
 <211> 3218  
 <212> DNA  
 <213> homo sapiens  
 <400> 391

Missing mandatory <220> to <223> features  
 to explain the "n's" at the circled  
 locations in the sequence. See #10 on

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gcgaccacga gctggtgcat ccatcagtag ccttgccgga ctttccctta aagaaggaga 60
ggatcagaaa gagataaaga ttgagccagc tcaggctgtg gatgaagtgg aacctctacc 120
tgaagactat tatacaagac cagtaaattt aacagaggta acaacccttc agcagcgtct 180
gttacagcct gacttccagc cagtctgtgc ttcacagctc tatcctcgcc acaaacatct 240
tctgatcaaa cggtccttgc gctgccgtaa atgtgaacat aatttgagca agccagaatt 300
taaccaaacg tcaatcaaat tcaaaatcca gctggctcgt gtcaattata ttccagaagt 360
gagaatcatg tcaattccca accttcgcta catgaaggag agccagggtc tcctgactct 420
tacaaatcca gttgagaacc tcacccatgt gactctcttc gagtgtgagg agggggacc 480
tgatgatata aacagcactg ctaagggtgt ggtgcctccc aaagagctcg ttttagctgg 540
caaggatgca gcagcagagt acgatgagtt ggcagaacct caagactttc aggacgatcc 600
tgacattata gccttcagaa aggccaacaa agtgggtatt ttcacaaag ttacaccaca 660
gcgtgaggag ggtgaagtga ccgtgtgctt caagatgaag catgatttta aaaacctggc 720
agccccatt cgccccattg aagaaagtga ccagggaaca gaagtcattt ggctcacc 780
gcatgtggaa cttagcttgg gccacttct tccttaaaag gttccactgg agggcagatc 840
ccaaaggaca gtatcaccgt aaacctgctg taaaatgtgg aagctgctgc ttcattaggc 900
cttgtttata acgatgtacc catgcactac ggaattctat tgctaagaaa gtgggagcat 960
aggcaaggca ttgggaacac agggtagctg ctgttgctct tgctctcacc cctgttgaca 1020
ccagtaagtc tgtgtctccc tcaactgaacc ctgcacgttg agtaacagca gcataattcc 1080
atcctaggaa aggggatggg tgttccttgg aatggcattg tatttaccac ctgagaaact 1140
ctgtactgtc tcttgatctg atctcactaa ggatcacaat gtcacagatg aaacttaa 1200
gataacccaa aggtagacct gctgttaatg atccagcatt ggtcacaatg taccaactgc 1260
tttctgcatt cgtttaaata tcatctaaca gtctaaaaca tatcccttca ttgccataat 1320
ggctgccatt ttgccataga ttcccatata actgaaaaac tgaattgtca ctttatcttt 1380
agtatcatga tgattggaaa aacctgtgaa gttgttaagg cactctcatt tgccctcttt 1440
ttctaagtga atacaggaca cgtattagtt gttcttaann nnnnnnnnnn nnnnnnnnnn 1500
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1560

```

the Error  
 Summary  
 Sheet

✓ F.Y.I.

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/673,840

DATE: 02/15/2001  
TIME: 14:19:56

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:132 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:  
L:319 M:283 W: Missing Blank Line separator, <400> field identifier  
L:320 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:  
L:323 M:283 W: Missing Blank Line separator, <400> field identifier  
L:324 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (11) SEQUENCE:  
L:449 M:283 W: Missing Blank Line separator, <400> field identifier  
L:450 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:  
L:453 M:283 W: Missing Blank Line separator, <400> field identifier  
L:454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:  
L:530 M:283 W: Missing Blank Line separator, <400> field identifier  
L:531 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
L:716 M:283 W: Missing Blank Line separator, <400> field identifier  
L:717 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:  
L:1039 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1040 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (41) SEQUENCE:  
L:1043 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1044 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (42) SEQUENCE:  
L:1083 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1084 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:  
L:1140 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1141 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:  
L:1444 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1445 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (64) SEQUENCE:  
L:1470 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1471 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:  
L:1486 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1487 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:  
L:1533 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1534 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:  
L:1537 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1538 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (71) SEQUENCE:  
L:1611 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1612 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:  
L:1636 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1637 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:  
L:1741 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1742 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (81) SEQUENCE:  
L:1785 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1786 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (84) SEQUENCE:  
L:1815 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1816 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (87) SEQUENCE:  
L:1842 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1843 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (89) SEQUENCE:  
L:1869 M:283 W: Missing Blank Line separator, <400> field identifier  
L:1870 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (91) SEQUENCE:

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/673,840

DATE: 02/15/2001  
TIME: 14:19:56

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

L:3227 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3228 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (130) SEQUENCE:  
L:3438 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3439 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (140) SEQUENCE:  
L:3442 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3443 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (141) SEQUENCE:  
L:3446 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3447 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (142) SEQUENCE:  
L:4427 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4428 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (175) SEQUENCE:  
L:4431 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4432 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (176) SEQUENCE:  
L:4435 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4436 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (177) SEQUENCE:  
L:4439 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4440 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (178) SEQUENCE:  
L:4443 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4444 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (179) SEQUENCE:  
L:4447 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4448 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (180) SEQUENCE:  
L:4565 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4566 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (185) SEQUENCE:  
L:4569 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4570 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (186) SEQUENCE:  
L:4573 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4574 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (187) SEQUENCE:  
L:4777 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4778 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (197) SEQUENCE:  
L:4781 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4782 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (198) SEQUENCE:  
L:4785 M:283 W: Missing Blank Line separator, <400> field identifier  
L:4786 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (199) SEQUENCE:  
L:5607 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5608 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (230) SEQUENCE:  
L:5611 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5612 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (231) SEQUENCE:  
L:5615 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5616 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (232) SEQUENCE:  
L:5665 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5666 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (234) SEQUENCE:  
L:5669 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5670 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (235) SEQUENCE:  
L:5673 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5674 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (236) SEQUENCE:  
L:5734 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5735 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (240) SEQUENCE:  
L:5738 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5739 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (241) SEQUENCE:  
L:5742 M:283 W: Missing Blank Line separator, <400> field identifier

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/673,840DATE: 02/15/2001  
TIME: 14:19:56Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

L:5743 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (242) SEQUENCE:  
L:5826 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5827 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (245) SEQUENCE:  
L:5830 M:283 W: Missing Blank Line separator, <400> field identifier  
L:5831 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (246) SEQUENCE:  
L:9955 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:391  
L:9955 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:391  
L:9955 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:391  
L:9955 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:391  
L:9955 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:391  
L:9956 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:391  
L:9956 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:391  
L:9956 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:391  
L:9956 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:391  
M:340 Repeated in SeqNo=391  
L:10173 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:396  
L:10173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:396  
L:10173 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:396  
L:10173 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:396  
L:10173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:396  
L:10193 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10193 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10193 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10193 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10193 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:397  
L:10195 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10195 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10195 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
M:340 Repeated in SeqNo=397  
L:10197 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10197 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10197 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10197 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10198 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10198 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10198 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10199 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10199 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10199 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10199 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10200 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10200 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10200 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10200 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10201 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10201 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10201 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397



VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/673,840

DATE: 02/15/2001  
TIME: 14:19:56

Input Set : A:\ES.txt  
Output Set: N:\CRF3\02152001\I673840.raw

L:10201 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10202 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10202 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10202 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10202 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10203 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10203 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:10203 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:397  
L:10203 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:397  
L:10204 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:397  
L:10204 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:397  
L:11013 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:11016 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:11019 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:11022 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:11025 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:11028 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:11031 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:11037 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:11047 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:11050 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:11053 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:11056 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4  
L:11059 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2